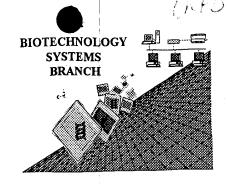
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/409, 800ASource: 1645Date Processed by STIC: 4/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

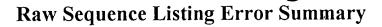
Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

CRE



KFF D

	ERROR DETECTED	SUGGESTED	CORRECTION	S	ERIAL NUMBER: 07	1909,00017
ATTN:	NEW RULES CASES: PI	.EASE DISREGAF	RD ENGLISH "ALPH	A" HEADERS, WHIC	H WERE INSERTED BY P	TO SOFTWARE
1	Wrapped Nucleics	The number/text a	at the end of each line	"wrapped" down to th	ie next line.	*
	.,		your file was retrieved			
		Please adjust you	ur right margin to .3, a	s this will prevent "wra	apping".	
2	Wrapped Aminos	The amino acid n	umber/text at the end	of each line "wrapped	" down to the next line.	
	.,		d in a word processor			
		Please adjust you	ur right margin to .3, a	s this will prevent "wra	apping".	
з 🔽	Incorrect Line Length	The rules require	that a line not exceed	72 characters in leng	th. This includes spaces.	
4	Misaligned Amino Acid	The numbering u	is may be caused by the use	e of tabs		
	Numbering	between the num	bering. It is recommen	nded to delete any tab	s and use spacing between	the numbers.
5	Non-ASCII	This file was not	saved in ASCII (DOS)	text, as required by t	he Sequence Rules.	
					Il text so that it can be proce	essed.
6	Variable Length	Sequence(s)	_ contain n's or Xaa's	which represented m	ore than one residue.	
			each n or Xaa can onl			
		•	ne maximum number o			
		indicate in the (ix	() feature section that s	some may be missing	i•	
7	Patentin ver. 2.0 "bug"	A "bug" in Patent	In version 2.0 has cau	used the <220>-<223	> section to be missing from	amino acid
	7 410111111 1011 1119				matically generate this section	
		previously coded	I nucleic acid sequenc	e. Please manually o	opy the relevant <220>-<22	3> section
		to the subsequer	nt amino acid sequenc	e. This applies prin	narily to the mandatory <2	220>-<223>
		sections for Art	ificial or Unknown so	equences.		
8	Skipped Sequences	Sequence(s)	_ missing. If intention	al, please use the follo	owing format for each skippe	ed sequence:
	(OLD RULES)		ON FOR SEQ ID NO:)			
					adings under "SEQUENCE	CHARACTERISTICS")
		· ·	DESCRIPTION:SEQ			
		This sequence i	is intentionally skipp	ped		
		Please also adjus	st the "(iii) NUMBER C	OF SEQUENCES:" re	sponse to include the skipp	ed sequence(s).
9	Skipped Sequences	Sequence(s)	missing. If intention	al, please use the follo	owing format for each skippe	ed sequence.
	(NEW RULES)	<210> sequenc	e id number			
		<400> sequenc	e id number			
		000	•			
10	Use of n's or Xaa's	Use of n's and/or	r Xaa's have been dete	ected in the Sequence	Listing.	
	(NEW RULES)		<223> is MANDATOF			
		In <220> to <223	section, please expl	lain location of n or X	aa, and which residue n or I	Xaa represents.
11	Use of "Artificial"	Use of "Artificial"	only as "<213> Orga	nism" response is inc	omplete, per 1.823(b) of Ne	w Sequence Rules.
	(NEW RULES)	Valid response i	s Artificial Sequence.			
12	Use of <220>Feature	Sequence(s)	_ are missing the <22	20>Feature and assoc	ciated headings.	
	(NEW RULES)				SM is "Artificial Sequence" o	or "Unknown"
		•	source of genetic ma			
		(See "Federa	al Register," 6/01	/98, Vol. 63, No.	104, pp. 29631-32)	(Sec. 1.823 of new Rules
13	Patentin ver 2.0 "hug"	Please do not u	ise "Copy to Disk" fi	unction of Patentin	version 2.0. This causes a	corrupted

AMC - Biotechnology Systems Branch - 4/06/2001

file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Instead, please use "File Manager" or any other means to copy file to floppy disk.

Does Not Comply Corrected Diskette Needed

SEQUENCE LISTING

(1) GEN	m	molary					
			i) A	APPLICANT:	Blattner,		
5 Goldon do ho	there is	Burland, Valerie Rose, Debra J. Mayhew, George F. Perna, Nicole Perry, Robert D. Straley, Susan C. Fetherston, Jacquel Lindler, Luther E. Plano, Gregory V.	.ine D	DO N TAB " do ho in she	codes. The t process w CRF program		
		/ENTION: Plasmid DN	IA fro	om Yersinia Pe	estis		
	(iii) NUMBER OF SE	EQUENCES: 3					
(15)	(iv) CORRESPONDEN			RESSEE: Quarle STREET: 1 Sou	es & Brady uth Pinckney		
Street	20	more	(D) (E)	CITY: Madisor STATE: WI COUNTRY: US ZIP: 53701-21			
		(v) COMPUTER RE	v) COMPUTER READABLE FORM:				
				MEDIUM TYPE: COMPUTER: IBN			
compatible DOS/MS-DOS	25	<u> </u>		OPERATING SYS	 ·/*		
2007.10 200			(D)	SOFTWARE: Wo	rd Perfect 8.0		
00/400 000	(vi) CU	JRRENT APPLICATION		APPLICATION N	NUMBER:		
09/409,800	30			FILING DATE: CLASSIFICATION			
	(viii)	ATTORNEY/AGENT IN					
960296.9593 <u>9</u> —		(<u>-</u>	(B)	NAME: Seay, N REGISTRATION REFERENCE/DOO	NUMBER: 27386		
35	(ix) Ti	ELECOMMUNICATION IN	(A)	ATION: TELEPHONE: (600)			

his page shown as a sample of global orners

€9/409,800A

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Jelete 5

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100990

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

use upper-case letters

insert

(ii) MOLECULE TYPE: DNA (plasmid)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

creating Sequence

10

aaacagcccg gcgtgctgga gcgactggaa cgtgaggacg gtgtcattat ccaccagcgt 60 cgcgagtggc gcatgtacga tccggaaaca ggtaagctca cgacgaaggc cggaacgctc 120 tggggtctgc tgaagaaaat ccactgataa caccaaccac tgcggtgagt agccagctca 180

ccgcgcgcgt atctgggtca taaccactgt agtgagtaaa acggctgccg tggcatccgg 240 tatccactgt agtgagtaaa gtggtgatta tcgacttcac tatccactgt agagagtaaa 300

caggogttca ttcacagcaa acaaccacta tggagagtga tggaatgcga cctccagcgg 360

gtatccacta tggagagtaa accttcactg ttttcagcgg atgtctactc tccacagtgg 420

ataqtaaatc caqccaaccq attctqctct ccataqtqqa tagccaatag cgaagggagc 480

aacgataacc actatagaga gtggatttaa caagtcaccc agtgaccact aacctcgcag 540

cccttqtttc atctaggttt gtaaccacta acattcattt cgttatttga gcgctactgc 600

ctacagtggt tactattcgg ttgttgttac tcactacagt ggatagcgga cttcagataa 660

acaaaaggcc cactacagcg gaatagtgag cctttctact ctctacagtg attgggctat 720

ttqcqaqcct ttqccttqcq caqctcttcq agaatcqcca qttcttcctt gctcaacatg 780

accatctcac cgtctttttc ttcaggaaca acatcgatga tgtcctcctg accatcgcca 840

ggcaagttat cttcctgctc ttctggttct tccggcgcag ctttagttgg tggcaatgcc 900

gggcgtaact tcggccgcct atagtggatg atgaagtaga ccgagctgcc gcgcttcact 960

tcggtgtaat cgagatagcc gatctcccgc agctgctcca tcgccttcct gactgtcgcg 1020

ttctqqqtaa tqqtqcqqct qqttaaqtta agtctqqcqc qtaaqcqaqc caacqaqatt 1080

qqtqccqqqt caqqtqqcaa actttcqatq aatqtqtaqa qtqcctqqqc qqattctttt 1140

ctggagagtt cgttgattgc ccggagttgc agaagaacct ttttgtcgaa ctggtagagt 1200

tcgaaaatct taggatcagc ctgcagcgag accgtgtcgt tcttagtgct gtactttgct 1260

gtctgcacaa ggtgagttac gtaatactca tcagagcctt tactgcggaa tgagatagtg 1320

1 steed

(see ten 3 on Eva Summary Sheet)

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